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P#13

JUL 31 2001

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TECH CENTER 1600/2900

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/138,735

DATE: 07/05/2001

TIME: 11:22:57

Input Set : A:\PTO.txt

Output Set: N:\CRF3\07052001\I138735.raw

3 <110> APPLICANT: PARANHOS-BACCALA, Glaucia  
 4 LESENECHAL, Mylene  
 5 JOLIVET, Michel  
 7 <120> TITLE OF INVENTION: TRYPANOSOMA CRUZI ANTIGEN, GENE ENCODING THEREFOR AND  
 METHODS OF  
 8 DETECTING AND TREATING CHAGAS DISEASE  
 10 <130> FILE REFERENCE: WPB 36400B  
 12 <140> CURRENT APPLICATION NUMBER: US 09/138,735  
 13 <141> CURRENT FILING DATE: 1998-08-24  
 15 <150> PRIOR APPLICATION NUMBER: US 08/480,917  
 16 <151> PRIOR FILING DATE: 1995-06-07  
 18 <150> PRIOR APPLICATION NUMBER: FR 94/10132  
 19 <151> PRIOR FILING DATE: 1994-08-12  
 21 <160> NUMBER OF SEQ ID NOS: 13  
 23 <170> SOFTWARE: PatentIn version 3.0  
 25 <210> SEQ ID NO: 1  
 26 <211> LENGTH: 3402  
 27 <212> TYPE: DNA  
 28 <213> ORGANISM: Trypanosoma cruzi  
 30 <400> SEQUENCE: 1

ENTERED

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33	gaagtacttg ccgtttgtg tgggtgacga gacaacacac atcgagcggg aaaaaaaaaa	120
35	aaaaggaaat aaattaaatt aaattatttg ttcttgaat aggcaaaagaa gaagaagaag	180
37	aaaaggtgcg ggggaggggag gagaaagcga cacacacaca aaaaaaaaaa aaggaattgc	240
39	ggaaataaca acgcaaggcg cgacatgac cgtgacggtg gattgttca atcatgcgaa	300
41	gccgagcaac aatgaggggcc gcgtgtggtc tggacgcgc gcgcattttt acgaggtgcc	360
43	tgaggcgcag cgtgtgttgc cgattcgca gtttatctt gcctacacca tgaagcggcg	420
45	tcacgtgtcgtc cgtgtgttgc agcgctcgaa ctttttgaag ggcaccgtgc gggcacactc	480
47	aaagccattt catgcgttgc agttgttgc ttaccgcgtt aacgtcgacatcgctgg	540
49	gaagggggag ttcttcgtgt gggtgttgc ggttgcgtt gggcaagcc acggcaagcc	600
51	ggatctcgca gcccgcctca cagtgaaggt gtacttaag cttcaggatc ctgtcacaat	660
53	tccatgtttt tcttttttcaacgcggc gagtcagcg cctgtatctgc ttgtcccttta	720
55	cggaaacgcggc gggcaattt ttagcagctc ctccttgcatt gagcgttgc acgttgcatt	780
57	actggaggca acactacagc ggaatttgcac aaccctgcga accctgactc aaccggtag	840
59	tgagaacagt ttatgtccgc ttggctctgg cggatgttgc accttttacca cggaaaccaac	900
61	aatggtagcg gcatgcacat tacgaaaccc cagcactcca tcatggcg tttgcgaggg	960
63	ttagccagtgc aaggcattgc atctccgttgc cgcacccgtt gaggaaaatgc ttagtgcgtt	1020
65	cgtggccgcata tctacaaaag ggggtgttgc atggcttgc acgggtgttgc cagaacccaa	1080
67	tttgcgttgcgc aagttgttgc ttgtatggatc tattgtcgatc atggaaaggtt caccggaaac	1140
69	gttgcgttgcgc tttgcgttgcgc ggaagcgttgc ggcgttgcgc aacatgcatt cccctcataa	1200
71	cttacacttgc acacactaca ttagtgccttgc ttaggttgc cgttgcgtt tttgttca	1260
73	tcgtacagcc gacggtagtgc gctgttgcgc ttagtgcgttgc attgttgc cgttgcgtt	1320
75	tctccggccgc tccgcggcgg aagaacagca gccagccaa aaaacatcgatc tagtggcgac	1380
77	ggggaaaccc ggggtgttgc cctcgggcgc tgacggcg agtagcgttgc ataccaatac	1440
79	gacttctgcgc gctgttgcgc cccctgcattt accccctgtt ttagtgcgttgc ccaaggcgc	1500
81	cgccgcctccgc gccgcggcgc gatcggttgc gccgcacgtt gggagcaaga tcattgttca	1560
83	tctagtgttgc cagtcgttgcgc ttagtgcgttgc ccaaggcgc gtcgttgcgc ctggagcgc	1620
85	ggccacgcgc aggttgcgttgc cgcgttgcgc cccctgcattt gaaacatcgatc tagtggcgac	1680

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87	atacggcac	aatggccgac	ctgtgacggc	tggattggtg	gcagctaata	gtggtgccag	1740										
89	cgcggcctcg	tctcccacag	ccgcggcgaa	accaacagga	gaagaaaaagg	cctccgccc	1800										
91	atgtgaaacg	agctccgtgg	cgataaaatgc	gacacgcccc	gcgcttcaca	acgcctctct	1860										
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95	tcatcagtcg	ctggagcggc	tgagatccgt	cataaccaac	acgtctcggg	ttctgaagtt	1980										
97	gctccctgac	accattcgaa	gagaccatga	acaacttctg	aatctgggtt	tagaggcaca	2040										
99	gatgacagag	ctgcagcaga	gccgtccaac	accgcaaaca	cagccgagag	acacaagctc	2100										
101	cgcgaaatca	tccgttgg	agacgtacac	ccttgcattc	attgcggatt	ccctctctcg	2160										
103	caacatcact	aagggggtga	agcgtgggt	gaacgaggcc	attatgtgc	atctcgacca	2220										
105	tgaggtgcgg	cacgcctatag	gaaaccggct	tcggcaaca	caaagaaca	tcatcaagag	2280										
107	ccgcctcgat	gaagcgttga	aggaaagcac	tacacagtt	acggctcaat	tgacgcaaac	2340										
109	ggtggagaat	ctggtaagc	gcgagcttc	cgaggtgtt	ggtagcatca	acggctccct	2400										
111	cacttctctc	gtgaaggaaa	atgcctcatt	acagaagag	ttgaattcca	taatgtctag	2460										
113	tgggtgtt	gatgaaatgc	gtcgtatgcg	ggaagagctg	tgacatattgc	gagagtccgt	2520										
115	tgcgaagcgg	aaggcaacaa	tgccagattc	ttcttcac	gccacgagct	ccttcaagg	2580										
117	aagaaggtct	gcgcccggaga	caattcttc	aaccgcgtt	tcgatggtg	gagagcagca	2640										
119	ataccgtca	ggactggaat	acatgttgc	ggctcagcag	ccctctctcc	tcctgcgggt	2700										
121	cctcagcata	cttacaagg	aaaacgaaa	cgcctactcg	gaacttattt	aaaatgtaga	2760										
123	gacgcgaat	gacgtgtgg	tttcgggtt	gttgcactc	atagagggc	cggcgaccga	2820										
125	ggctgagaag	gagggtgtt	ttggcgtcgc	cattgatatt	ctctccgagc	gcgatcaa	2880										
127	tgctcagaac	ggcgcactcg	gctcgaaact	caccacggc	atgcgagcct	ttgagcgaca	2940										
129	ggcaaggtcg	gagacaacga	gcaggtcatt	cttgcataatgc	ctgaaagaacc	tggaaaagct	3000										
131	tctgcataatca	tgataataaa	aagaactcaa	cgaatacagt	tggtgattat	taaggaaggg	3060										
133	aaaagagaga	aagagagaga	gagagagaga	aatgtatgg	gcgttttagtt	acggtagaaa	3120										
135	aaaaacgtgt	ggataagaag	gagggtttt	gtgtgcgacc	aggaattact	ggggAACGCT	3180										
137	gctacacggc	ggaatcgacc	attttattt	tatttattt	gtcttttagta	ttatgttttt	3240										
139	tcttgtgtgt	gtgtgtgtgt	gttttgtgtgt	gtgcggttat	tttgtatccg	tttgtcccg	3300										
141	cccctgcccc	ccatcacccg	aggagaaagt	agaataagac	acatacgtt	gttgttttg	3360										
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151	<400>	SEQUENCE:	2														
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156	Glu	Gly	Arg	Val	Trp	Ser	Val	Asp	Ala	Ala	Thr	Phe	Asn	Glu	Val	Pro	
157					20			25				30					
159	Glu	Ala	Gln	Arg	Val	Leu	Ala	Asp	Ser	Gln	Phe	Tyr	Leu	Ala	Tyr	Thr	
160					35			40				45					
162	Met	Lys	Arg	Arg	His	Val	Leu	Arg	Val	Val	Lys	Arg	Ser	Asn	Leu	Leu	
163		50			55			60									
165	Lys	Gly	Thr	Val	Arg	Ala	His	Ser	Lys	Pro	Ile	His	Ala	Val	Lys	Phe	
166		65			70			75				80					
168	Val	Asn	Tyr	Arg	Ser	Asn	Val	Ala	Ala	Ser	Ala	Gly	Lys	Gly	Glu	Phe	
169		85			90			95									
171	Phe	Val	Trp	Val	Val	Thr	Asp	Glu	Thr	Asp	Ala	Ser	Asn	Gly	Lys	Pro	
172		100			105			110									
174	Asp	Leu	Ala	Ala	Arg	Leu	Thr	Val	Lys	Val	Tyr	Phe	Lys	Leu	Gln	Asp	

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175	115	120	125
177	Pro Val Thr Ile Pro Cys Phe Ser Phe Phe Ile Asn Ala Glu Ser Gln		
178	130	135	140
180	Arg Pro Asp Leu Leu Val Leu Tyr Glu Thr Gln Ala Ala Ile Leu Asp		
181	145	150	155
183	Ser Ser Ser Leu Ile Glu Arg Phe Asp Val Glu Ser Leu Glu Ala Thr		
184	165	170	175
186	Leu Gln Arg Asn Cys Thr Thr Leu Arg Thr Leu Thr Gln Pro Val Ser		
187	180	185	190
189	Glu Asn Ser Leu Cys Ser Val Gly Ser Gly Gly Trp Phe Thr Phe Thr		
190	195	200	205
192	Thr Glu Pro Thr Met Val Ala Ala Cys Thr Leu Arg Asn Arg Ser Thr		
193	210	215	220
195	Pro Ser Trp Ala Cys Cys Glu Gly Glu Pro Val Lys Ala Leu His Leu		
196	225	230	235
198	Leu Asp Ala Thr Val Glu Glu Asn Val Ser Val Leu Val Ala Ala Ser		
199	245	250	255
201	Thr Lys Gly Val Tyr Gln Trp Leu Leu Thr Gly Val Ala Glu Pro Asn		
202	260	265	270
204	Leu Leu Arg Lys Phe Val Ile Asp Gly Ser Ile Val Ala Met Glu Ser		
205	275	280	285
207	Ser Arg Glu Thr Phe Ala Val Phe Asp Asp Arg Lys Gln Leu Ala Leu		
208	290	295	300
210	Val Asn Met His Ser Pro His Asn Phe Thr Cys Thr His Tyr Met Met		
211	305	310	315
213	320	325	330
214	335		
216	Gly Ser Cys Val Leu Ala Asp Met Ser Asn Arg Leu Thr Ile Phe His		
217	340	345	350
219	Leu Arg Cys Ser Arg Arg Glu Glu Gln Gln Pro Gly Gln Lys Thr Ser		
220	355	360	365
222	Val Val Ala Thr Ala Lys Pro Gly Cys Val Ser Ser Gly Thr Asp Ala		
223	370	375	380
225	Ala Ser Ser Ser His Thr Asn Thr Thr Ser Ala Ala Ala Ser Pro		
226	385	390	395
228	400	405	410
229	415		
231	Ala Ala Arg Ser Ala Glu Pro His Val Gly Ser Lys Ile Ile Ala Asn		
232	420	425	430
234	Leu Val Asn Gln Leu Gly Ile Asn Val Thr Gln Arg Ser Val Val Ser		
235	435	440	445
237	Thr Gly Ala Pro Ala Thr Thr Arg Ser Thr Ala Val Thr Ser Thr Thr		
238	450	455	460
240	460	470	475
241	480		
243	485	490	495
244	500	505	510

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249 Cys Glu Thr Ser Ser Val Ala Ile Asn Ala Thr Arg Pro Ala Leu His  
 250 515 520 525  
 252 Asn Ala Ser Leu Pro Gln Ala Pro Thr Asp Gly Val Leu Ala Ala Ala  
 253 530 535 540  
 255 Val Tyr Gln Ser Glu Gly Glu Val His Gln Ser Leu Glu Arg Leu Glu  
 256 545 550 555 560  
 258 Ser Val Ile Thr Asn Thr Ser Arg Val Leu Lys Leu Leu Pro Asp Thr  
 259 565 570 575  
 261 Ile Arg Arg Asp His Glu Gln Leu Leu Asn Leu Gly Leu Glu Ala Gln  
 262 580 585 590  
 264 Met Thr Glu Leu Gln Gln Ser Arg Pro Thr Pro Gln Thr Gln Pro Arg  
 265 595 600 605  
 267 Asp Thr Ser Ser Ala Lys Ser Ser Val Phe Glu Thr Tyr Thr Leu Val  
 268 610 615 620  
 270 Leu Ile Ala Asp Ser Leu Ser Arg Asn Ile Thr Lys Gly Val Lys Arg  
 271 625 630 635 640  
 273 Gly Val Asn Glu Ala Ile Met Leu His Leu Asp His Glu Val Arg His  
 274 645 650 655  
 276 Ala Ile Gly Asn Arg Leu Arg Gln Thr Gln Lys Asn Ile Ile Lys Ser  
 277 660 665 670  
 279 Arg Leu Asp Glu Ala Leu Lys Glu Ser Thr Thr Gln Phe Thr Ala Gln  
 280 675 680 685  
 282 Leu Thr Gln Thr Val Glu Asn Leu Val Lys Arg Glu Leu Ala Glu Val  
 283 690 695 700  
 285 Leu Gly Ser Ile Asn Gly Ser Leu Thr Ser Leu Val Lys Glu Asn Ala  
 286 705 710 715 720  
 288 Ser Leu Lys Lys Glu Leu Asn Ser Ile Met Ser Ser Gly Val Leu Asp  
 289 725 730 735  
 291 Glu Met Arg Arg Met Arg Glu Glu Leu Cys Thr Leu Arg Glu Ser Val  
 292 740 745 750  
 294 Ala Lys Arg Lys Ala Thr Met Pro Asp Ser Ser Leu His Ala Thr Ser  
 295 755 760 765  
 297 Ser Phe Gln^Gly Arg Arg Ser Ala Pro Glu Thr Ile Leu Ala Thr Ala  
 298 770 775 780 ^  
 300 Leu Ser Met Val Arg Glu Gln Gln Tyr Arg Gln Gly Leu Glu Val Met  
 301 785 790 795 800  
 303 Leu Met Ala Gln Gln Pro Ser Leu Leu Leu Arg Phe Leu Ser Ile Leu  
 304 805 810 815  
 306 Thr Arg Glu Asn Glu Asn Ala Tyr Ser Glu Leu Ile Glu Asn Val Glu  
 307 820 825 830  
 309 Thr Pro Asn Asp Val Trp Cys Ser Val Leu Leu Gln Leu Ile Glu Ala  
 310 835 840 845  
 312 Ala Ala Thr Glu Ala Glu Lys Glu Val Val Val Gly Val Ala Ile Asp  
 313 850 855 860  
 315 Ile Leu Ser Glu Arg Asp Gln Ile Ala Gln Asn Gly Ala Leu Gly Ser  
 316 865 870 875 880  
 318 Lys Leu Thr Thr Ala Met Arg Ala Phe Glu Arg Gln Ala Arg Ser Glu  
 319 885 890 895  
 321 Thr Thr Ser Arg Ser Phe Leu Gln Cys Leu Lys Asn Leu Ile Lys Leu

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322	900	905	910
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325	915		
327	<210> SEQ ID NO: 3		
328	<211> LENGTH: 24		
329	<212> TYPE: DNA		
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332	<220> FEATURE:		
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VERIFICATION SUMMARY  
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L:366 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6  
L:378 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7  
L:390 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8  
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